

266 G|A|T|G|P|H|e|a|T|T|P|e|a|s|n|y|s|g|l|u|y|s|g|l|l|e|p|e|l|y|s|l|e|g| 282
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 633 G|C|C|C|G|T|T|A|T|C|C|G|C|T|C|A|C|A|G|A|G|A|A|G|C|A|T|C|T|C|A|A|A|T|T|G|A| 584
 282 u|A|S|P|S|e|T|A|G|l|u|V|A|l|A|A|T|G|l|e|u|T|P|G|l|Y|l|e|A|T|G|y|s|n|A|T|P|T|O|A| 299
 |||||||
 583 G|G|A|C|T|C|A|G|A|C|A|G|T|G|C|C|G|C|A|C|T|G|G|G|G|T|G|G|C|A|G|A|A|C|G|C|C|A|G| 534
 299 l|A|e|T|A|s|n|T|y|A|s|P|l|y|s|L|e|u|S|e|A|T|G|S|e|T|l|e|A|T|G|l|n|T|T|y|T|l|y|s| 315
 |||||||
 533 C|C|A|T|G|A|A|C|T|A|T|G|A|A|C|T|A|A|C|C|C|C|C|A|T|C|C|C|C|A|T|A|C|A|G|A|G| 484
 316 G|Y|l|l|e|l|e|A|T|G|l|y|P|T|A|S|P|l|e|S|e|T|A|T|G|l|e|u|V|A|l|T|T|G|l|n|P|H|e|V|A| 332
 |||||||
 483 G|G|C|A|T|A|T|T|C|G|T|A|A|C|C|G|A|C|A|T|T|C|T|G|C|C|C|T|T|T|C|T|A|A|T|T|G|T| 434
 332 l|H|S|P|T|O|l|e| 335
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 433 G|C|A|T|C|C|A|G|T|C| 424
 seq_name: gb_est13-AA930371

seq_documentation_block: 504 bp mRNA EST 23-APR-1998
 LOCUS AA930371
 DEFINITION v045a05.r1 Barstead mouse irradiated colon MRLB7 Mus musculus cDNA
 clone IMAGE:1052816 5' similar to SM:ETS4-DROME P29775 DNA-BINDING
 PROTEIN D-ETS-4 ; mRNA sequence.
 ACCESSION AA930371 GI:3079964
 VERSION AA930371.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 504)
 Maira, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, I.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, H.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LHM, contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:584392

Seq primer: -28m3 rev2 ET from Amersham
 High quality sequence stop: 496.

FEATURES
 source
 1. 504
 Location/Qualifiers

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:1052816"
 /clone_lib="Barstead mouse irradiated colon MRLB7"
 /dev_stage="8 weeks"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained
 from 8 week old mouse. Colon was harvested 72 hours after
 irradiation with 1400 Gys. 1st strand cDNA was primed
 with a Not I - oligo(dT) primer
 15'TGTACAGATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
 T 3'; double-stranded cDNA was ligated to Eco RI
 adaptors [AATCGCATCTTG], digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73

vector. Library constructed by Rob Barstead.
 BASE COUNT 122 a 149 c 135 g 98 t
 ORIGIN
 alignment_scores:
 Quality: 548.00 Length: 104
 Ratio: 5.269 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 96.154
 alignment_block:
 US-09-126-945b-2 x AA930371 ..

Align seg 1/1 to: AA930371 from: 1 to: 504

232 G|U|G|U|S|E|T|T|P|H|A|S|P|S|e|T|G|l|u|V|A|l|S|e|T|C|y|S|e|S|e|T|G|l|n|P| 248
 |||||||
 1 G|A|G|A|G|G|G|T|T|C|A|G|T|G|A|G|T|G|A|G|T|G|G|T|G|G|T|G|G|T|G|G|T|G|G|T|G|G|T| 50
 248 o|l|e|h|e|l|e|u|T|P|G|l|n|P|H|e|u|S|g|l|u|e|l|e|u|S|P|H|S|e|T| 245
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 51 C|A|T|C|A|C|T|G|T|G|C|A|C|T|T|C|T|G|A|A|G|A|A|C|T|G|T|C|A|G|C|C|C|A|C|A|G|T| 100
 245 Y|C|I|A|T|P|H|e|a|T|T|P|e|a|s|n|y|s|g|l|u|y|s|g|l|l|e|p|e|l|y|s|l|e|g| 282
 |||||||
 101 A|U|G|C|C|G|C|T|C|A|C|G|C|T|G|G|C|C|A|A|A|A|G|C|A|A|G|C|A|C|T|T|C|A|A|A|A|T| 150
 282 G|U|A|S|P|S|e|T|A|G|l|u|V|A|l|A|A|T|G|l|e|u|T|P|G|l|Y|l|e|A|T|G|y|s|n|A|T|P|T|O|A| 299
 |||||||
 151 G|G|A|G|A|T|C|A|G|A|C|A|G|T|G|C|C|G|C|A|C|T|T|G|G|G|G|T|G|G|C|A|G|A|A|C|G|C|C|A|G| 200
 299 o|A|l|e|T|A|s|n|T|y|A|s|P|l|y|s|L|e|u|S|e|A|T|G|S|e|T|l|e|A|T|G|l|n|T|T|y|T|l|y|s| 315
 |||||||
 201 A|A|C|C|A|T|G|A|A|C|T|A|T|G|A|A|C|T|A|A|C|C|C|C|A|T|C|C|C|C|A|T|A|C|A|A|A| 250
 315 Y|C|I|A|T|P|H|e|a|T|T|P|e|a|s|n|y|s|g|l|u|y|s|g|l|l|e|p|e|l|y|s|l|e|g| 341
 |||||||
 251 A|G|G|C|A|T|A|T|T|C|G|T|A|A|C|C|G|A|C|A|T|C|T|G|A|G|C|C|C|T|T|G|T|A|C|C|A|A|T|T| 300
 332 V|A|H|S|P|T|O|l|e| 335
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 301 G|T|C|A|T|C|C|A|G|T|C| 312

seq_name: gb_est189-BF535871

seq_documentation_block: 637 bp mRNA EST 11-DEC-2000

LOCUS BF535871
 DEFINITION 602051384F1 NCI_CGAP_S52 Mus musculus cDNA clone IMAGE:419037 5',
 mRNA sequence.

ACCESSION BF535871
 VERSION BF535871.1 GI:11023239
 KEYWORDS EST.

SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 637)
 NIH M23 HTP-99-0-1 with 9999
 Mammalian: Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Mus.

TITLE NIH M23 HTP-99-0-1 with 9999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rstraus@nsl.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LHM)
 DNA Sequencing by: Invitro Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LHM at:
 http://image.llnl.gov

plate: LL4951a row: 9 column: 22
 High quality sequence stop: 637.
 Location/Qualifiers

FEATURES
 source
 1. 637



00:01:05-09:126-945b-2 LOG EST: * out-format: .fts
 Date: Sep 18, 2001 6:43 AM

Alert: Results were produced by the Gensico software, version 1.5.
 Copyright (c) 1993-2000 Compuser Inc.

Command line parameters:

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 -DB=EST_QEFT fastap -SUFFIX=ft -CAPOPT=12,000 -CAEXT=4,000
 -MINMATCH=0.100 -LAPOPT=0.000 -LAPEXT=0.000 -CAPAP=6,000
 -CAPAP=0.050 -XAPAP=0.000 -YCAPEXT=0.500 -PECAP=6,000
 -DEEXT=7,000 -YAPAP=10,000 -YCAPEXT=0.500 -DELDP=6,000
 -LIST=150 -LOCAL=000 -HIS=SCORE.PPT -HIS_MAX=100 -HIS_MIN=0
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 -LPOU=1 -LONGJOB=NO -LXPLY=WAIT -THREADS=1

Search information block:

Query: US-09-126-945b-2
 Query length: 145
 Database: EST
 Database sequence: 10228115
 Database length: 43459454
 Search time (sec): 1464.200000

Score list:

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db_08143:AM079479      * 200.00 349.84 1.0e-08 477 1AM079479 1M0101065 120100-001
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db_08131:AM1209884      * 200.00 345.64 1.8e-08 673 1AM1209884 A01209884 N26E22 Hmns
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db_08115:AI1034744     * 199.50 325.02 5.5e-09 291 1AI1034744 352521211 Sources: mmm
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db_08125:AI794162      * 199.00 345.46 1.7e-08 554 1AI794162 3051009 Y5 N1 CGAP:50
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db_08150:AM057616      * 199.00 346.21 1.7e-08 561 1AM057616 110841 MARC:110
db_08189:BE084050      * 199.00 343.84 2.3e-08 682 1BE084050 6020962961 N1 CGAP:50
db_08140:AV034666      * 199.00 343.24 2.5e-08 712 1AV034666 AV034666 CDA Hmns: zap
db_08113:AM019938      * 198.50 347.99 1.4e-08 468 1AM019938 60180554E1 N1 CGAP:50
db_08184:BM081270      * 198.50 346.69 1.7e-08 504 1BM081270 60180554E1 N1 CGAP:50
db_08121:AI958412      * 198.50 345.10 1.7e-08 529 1AI958412 1128410241 N1 CGAP:50
db_08112:AM015785      * 198.50 345.51 1.9e-08 555 1AM015785 60180554E1 N1 CGAP:50
db_08149:AM001848      * 198.50 344.44 3.2e-08 777 1AM001848 60180554E1 N1 CGAP:50
db_08184:BE143562      * 198.50 341.42 4.3e-08 945 1BE143562 601790916E1 N1 CGAP:50
db_08184:BE143562      * 198.50 341.42 4.3e-08 945 1BE143562 601790916E1 N1 CGAP:50
db_08164:AV192171      * 197.50 349.13 1.2e-08 460 1AV192171 AV192171 Y0J1 Kohata: 0
db_08176:BE19674      * 197.50 348.54 1.3e-08 478 1BE19674 60180554E1 N1 CGAP:50
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db_08190:BM0604437     * 197.50 345.20 1.8e-08 478 1BM0604437 268948 MARC:300V B08
db_08193:BM062778      * 197.50 345.55 1.9e-08 483 1BM062778 60180554E1 N1 CGAP:50
db_08153:AM041181      * 197.50 343.48 2.1e-08 519 1AM041181 60180554E1 N1 CGAP:50
db_08171:BE191776      * 197.50 343.28 2.5e-08 582 1BE191776 60180554E1 N1 CGAP:50
db_08129:AI587001      * 197.50 342.05 2.9e-08 644 1AI587001 AI587001 S101:adeno: 0
db_08102:BE057609      * 197.50 341.81 3.0e-08 657 1BE057609 6020962961 N1 CGAP:50
db_08196:BE060494      * 197.50 341.18 3.4e-08 692 1BE060494 6019110241 N1 CGAP:50
db_08196:BE060494      * 197.50 341.18 3.4e-08 692 1BE060494 6019110241 N1 CGAP:50
db_08129:AI571262      * 197.50 342.53 5.2e-08 934 1AI571262 AI571262 L11 NIH006 JH
db_08110:BM0420378     * 197.50 306.99 5.0e-08 976 1BM0420378 602452437E1 NIH-MD XRG

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seq name: db_08197:BM079568

seq document block:

LOCUS: BM079568 991 bp mRNA EST 06 FEB 2001
DEFINITION: 60242818/21 NIH-MD XRG Homo sapiens cDNA clone: IMAGE:4429413 5'.

ACCESSION: mRNA sequence.

VERSION: BM079568.1 GI:12686271

KEYWORDS: EST

SOURCE: human.

ORGANISM: Homo sapiens

EXTRACTOR: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Eckerpoda: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE: 1 (bases 1 to 991)

1116 NIH-MD Inst/Hp/2000 not with gov/

JOURNAL: National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT: Published (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: eap@nih.gov

TISSUE: Prostate

CDNA LIBRARY: Prepared from: Date: Technologies, Inc.

CDNA SEQUENCING BY: The J. M. A. G. E. Consortium (J.M.A.G.E.)

CLONE DISTRIBUTION: MGC clone distribution information can be found through the J. M. A. G. E. Consortium/J.M.A.G.E. at:

http://imgc.nih.gov

PLATE: HAM0181 row: d column: 22

High quality sequence slope: 655.

Location/Qualifiers

1..991

Organization: "Homo sapiens"

db_xref: "taxon:9606"

Location: "IMAGE:4429413"

Location: "NIH-MD XRG"

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Accession: "us-09-126-945b-2.rst"

Percent Similarity:	49.684	Percent Identity:	46.111
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411	411
10	GAGNNGSTWAS.....	10	WAGNNGSATGCTTCTCTCTGAGGAGGAGG
248	GIHQIASEETPIIRASPSGCIHVALASPSSETSEYSSGSGIYGLIHT	255	GIHQIASEETPIIRASPSGCIHVALASPSSETSEYSSGSGIYGLIHT
411	411
64	GATCATCTCTGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	64	GATCATCTCTGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
265	YTGIVAIAPHLIQAATPIPLQASLYSGIHLYS.....	276	YTGIVAIAPHLIQAATPIPLQASLYSGIHLYS.....
114	AGGGAGCTGCAATGCTGCTGGCTGAACCAAGCAAGCAAGCAAGCAAG	114	AGGGAGCTGCAATGCTGCTGGCTGAACCAAGCAAGCAAGCAAGCAAG
276	276
154	TCCTGTATGTTTAACTTAAAGATACATCTTAAATGIGCTGTGGA	201	TCCTGTATGTTTAACTTAAAGATACATCTTAAATGIGCTGTGGA
276	276
204	GGAGGAGCTGATCTGTACACACCAATACATTAACCAAGCAAGCAAG	255	GGAGGAGCTGATCTGTACACACCAATACATTAACCAAGCAAGCAAG
276	276
254	ALGCAAAATGTAIGTTCTCTTATTAATTCCTATTAATTAATTAAGTAC	300	ALGCAAAATGTAIGTTCTCTTATTAATTCCTATTAATTAATTAAGTAC
276	276
404	GAATACATTTCAAAAAAATAATTAAGTCTGTGTAATATATATCTCT	451	GAATACATTTCAAAAAAATAATTAAGTCTGTGTAATATATATCTCT
276	276
454	ETGATATATCTTAGTATAAATTTAATTTAAAGATTTCTTAAAT	400	ETGATATATCTTAGTATAAATTTAATTTAAAGATTTCTTAAAT
276	276
404	AGAAATATATACAAATCTCAAAACCAATGCTTTGCTATTGTTTCT	451	AGAAATATATACAAATCTCAAAACCAATGCTTTGCTATTGTTTCT
276	276
454	ATTTTATAAGTAGTACGTCTGAATCTAGTTTAAATAAATGAAACCT	500	ATTTTATAAGTAGTACGTCTGAATCTAGTTTAAATAAATGAAACCT
276	276
504	ATGCAAAATATCAAAACCAATCTCTGAAGCTGTTTACGTCTTAA	554	ATGCAAAATATCAAAACCAATCTCTGAAGCTGTTTACGTCTTAA
277	277
554	AAAAAGTACCTGTATCTCTCTCAAGATTTTAAATTAAGTATCT	603	AAAAAGTACCTGTATCTCTCTCAAGATTTTAAATTAAGTATCT
284	TAAGGIVAIADATGSEETFGIYGLIATLYSASATATATATATAT	301	TAAGGIVAIADATGSEETFGIYGLIATLYSASATATATATATAT
411	411
604	AAATGATCTGCTGATGCTTTTGGGGCTCTGCAAAATCTGATCTGATA	654	AAATGATCTGCTGATGCTTTTGGGGCTCTGCAAAATCTGATCTGATA
301	SGITGASPSYSEATASCTTAAAGCTTCTTCTTCTTCTTCTTCTTCT	317	SGITGASPSYSEATASCTTAAAGCTTCTTCTTCTTCTTCTTCTTCT
654	ATCATATATATCTGAGCTCTGATATCTGATATCTATATATATATAT	701	ATCATATATATCTGAGCTCTGATATCTGATATCTATATATATATAT
418	ATATGATGATATASPTTSEGTATATATGATATATCTTCTTCTTCT	438	ATATGATGATATASPTTSEGTATATATGATATATCTTCTTCTTCT
704	ATTCCTAAAGCTGATGCTGCTGATGATATGAGGATGAGCTGCTGAT	754	ATTCCTAAAGCTGATGCTGCTGATGATATGAGGATGAGCTGCTGAT
434	GLLE 345		
1111			
754	AGTG 757		

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seq.document.info.block:
ID:US      A1685592     486 bp      mRNA          EST       15,087-1999
DEFINITION: U022607.X1 NC_000467.p28 Homo sapiens cDNA clone IMAGE:251506, similar to contains FIBR14 MSK1 repetitive element 7; mRNA sequence.
ACCESSION  A1685592
KEYWORDS   A1685592.1 GI:486886
SOURCE     HSI
ORGANISM   human
Homo sapiens
Eukaryotic Metazoa Chordata Vertebrata Euteleostomi Mammalia Primates Catarrhini Hominoidea Homo.
REFERENCE  1 (bases 1 to 486)
AUTHOR    Kozaki T, et al.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Stansberg, Ph.D.  
Email: rstanber@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.; Michael R. Hammett-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bruno Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
RNA Sequenced by: Washington University Genome Sequencing Center  
Clone distribution: NC-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINCOLN at:  
www.lincoln-gov.org/cgare\_image.html  
Insert length: 1143 Std Error: 0.00  
Seq primer: -40bp from either  
High quality sequence stop: 480.  
Location/Qualifiers  
1..486  
/organism "Homo sapiens"  
/db_xref "taxon:9606"  
/clone "IMAGE:251506"  
/clone_lib "NC-CGAP_p128"  
/sex "male"  
/dev_stage "adult"  
/lab_host "H10B"  
/notes "Organ: prostate; Vector: pTZ19 Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NC-CGAP_p122 was prepared, and ss clones were made in vitro. Following BAP purification, this DNA was used as tracer in a substitution hybridization reaction. The driver was PCR amplified cDNAs from a pool of 5,000 clones made from the same library (clones 985608-986759, 1101192-1101959, and 1219428-1220615). Subcloning by Inco-Sources and M. Fatima Romaldo."
```


Seq primer: 28n13 rev2 ET from Amersham
 High quality sequence stop: 441.
 Location/Qualifiers

FEATURES

Source

1..555

/organism "Mus musculus"

/strain "M01947"

/clone "IMAGE:743447"

/colony_lib "Source mouse 48M12.5"

/tissue "embryo"

/tissue_type "Fetus"

/dev_stage "12.5dpc total fetus"

/lab_host "DH10B"

/note "Organ: whole fetus; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker site; Not I site 24 bp from 1st strand cDNA was primed with a Not I (3036G) primer [5'] TGTATTAATCTCAATGACGACGCGCTTAATTTTTTTTTTTTTTTT [3'] on total mouse RNA [provided by M. W. K. State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector; library went through one round of normalization, and was constructed by Benzo Soares and M. Patricia Bonaldo."

BASE COUNT

121 a 154 c 168 g 112 t

ORIGIN

alignment_scores:

Quality: 240.00 Length: 114
 Ratio: 2.771 Gaps: 6
 Percent Similarity: 72.807 Percent Identity: 45.614

alignment_block:

US-09-126-945b-2 x M261331 ..

Align seq 1/1 to: M261331 from: 1 to: 555

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221 ProGValAlLeHis...TyrGysAlaSerThrSerGluHisGlyPhe 266
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
57 GCGCAAGTTCGCGGAG...CTTGAGAGAGAAAGGTAATGCGACAT 104
111 111 111 111 111 111 111 111 111 111 111 111 111 111
236 TASPScGhValASPserSerGysSerGlyPro...LeuHisGlu 252
105 ....AATGCTGAGAGCTTCCTACATGACAGACATCTGAGATG 150
111 111 111 111 111 111 111 111 111 111 111 111 111 111
252 TPLPpSerGhGysSerGluGluGlyPhe...HisSerTyrGlyGlyPhe 268
111 111 111 111 111 111 111 111 111 111 111 111 111 111
151 GCGAGTTTCGCGGAG...CTTGAGAGAGAAAGGTAATGCGACAT 197
111 111 111 111 111 111 111 111 111 111 111 111 111 111
265 AGGValAlaGATGATGTCGlyLeuArgGysAsnArgProAlaMetAsn 302
111 111 111 111 111 111 111 111 111 111 111 111 111 111
248 GAGAGTTCGCGGAG...CTTGAGAGAGAAAGGTAATGCGACAT 297
111 111 111 111 111 111 111 111 111 111 111 111 111 111
302 GAGAGTTCGCGGAG...CTTGAGAGAGAAAGGTAATGCGACAT 347
111 111 111 111 111 111 111 111 111 111 111 111 111 111
298 AGGAGTTCGCGGAG...CTTGAGAGAGAAAGGTAATGCGACAT 347
111 111 111 111 111 111 111 111 111 111 111 111 111 111
319 ArgGysTrpGAPHisSerGluAlaGluValTyrGluPheVal 442
111 111 111 111 111 111 111 111 111 111 111 111 111 111
348 GCGCAAGTTCGCGGAG...CTTGAGAGAGAAAGGTAATGCGACAT 486
111 111 111 111 111 111 111 111 111 111 111 111 111 111

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seq_name: gb_cst100:hg193711

seq_document: hg193711 788 bp mRNA EST 12 Mar 2001
 DEFINITION: 602412140P1 NIH_MGC_92 Homo sapiens cDNA, clone IMAGE:743447, 555 bp
 mRNA sequence.
 ACCESSION: hg193711
 VERSION: hg193711.1 GI:13287159

KEYWORDS

EST

Source

ORGANISM

human.

Human Sapiens

Eukaryota; Metazoa; Chordata; Cephalochordata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;

Chimpanzee (1993)

National Institutes of Health; Human Genome Collection (MG)

GenBank (1993)

GenBank (1993)

GenBank (1993)

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[illegible][illegible]

seq name: gb-est28.A112095.1

seq document ation block:

LOCUS A112095.1 446 bp mRNA EST 25-FEB-2000
DEFINITION DKFZ762E04.1 762 (879-079) clone of RNA clone
DKFZ762E04.1 762 mRNA sequence.

ACCESSION

A112095.1 GI:15926952

VERSION

EST

KEYWORDS

EST

ORGANISM

human

REFERENCE

1 (bases 1 to 446)

AUTHORS

Kocher, K., Meyer, A., Moes, H. W., Gassmann, J., and Wiemann, S.

TITLE

EST (Kocher, et al.)

COMMENT

Am Klopfer, J. B. D-82192 Martinsried, Germany

FEATURES

source

1..446

organization "Homo sapiens"

24..300

24..300

24..300

24..300

24..300

24..300

24..300

24..300

24..300

24..300

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24..300

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24..300

24..300

24..300

24..300

24..300

24..300

259 GAAAGAAATATGCAAAAGATTC...ATTCAGACATATATGATTAAGACT 405

441 b-V41 442

11111

406 11010 410

seq name: gb-est76.BF554256

seq document ation block:

LOCUS BF554256 622 bp mRNA EST 15-APR-2000
DEFINITION BF554256 Not Eval. Mus musculus cDNA clone IMAGE:415002 57
similar to cDNA of 25. Mus musculus cDNA related protein M1 (MolSE).
mRNA sequence.

ACCESSION

BF554256.1 GI:10817724

VERSION

EST

KEYWORDS

EST

ORGANISM

house mouse

REFERENCE

1 (bases 1 to 622)

AUTHORS

Wang, A. H. P., et al.

TITLE

EST (Wang, et al.)

COMMENT

Am Klopfer, J. B. D-82192 Martinsried, Germany

FEATURES

source

1..622

organization "Mus musculus"

24..300

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24..300

[illegible][illegible]

US-04-126-945B-2 X AAA38342

Align Seq 1/1 to: AAA38342 from: 1 to: 2268

3	SerialiserProgl1LeuSerSerValSerProSerHisLeuLeuLeuP	13	103	108	113	118	123	128	133	138	143	148	153	158	163	168	173	178	183	188	193	198	203	208	213	218	223	228	233	238	243	248	253	258	263	268	273	278	283	288	293	298	303	308	313	318	323	328	333	338	343	348	353	358	363	368	373	378	383	388	393	398	403	408	413	418	423	428	433	438	443	448	453	458	463	468	473	478	483	488	493	498	503	508	513	518	523	528	533	538	543	548	553	558	563	568	573	578	583	588	593	598	603	608	613	618	623	628	633	638	643	648	653	658	663	668	673	678	683	688	693	698	703	708	713	718	723	728	733	738	743	748	753	758	763	768	773	778	783	788	793	798	803	808	813	818	823	828	833	838	843	848	853	858	863	868	873	878	883	888	893	898	903	908	913	918	923	928	933	938	943	948	953	958	963	968	973	978	983	988	993	998	1003	1008	1013	1018	1023	1028	1033	1038	1043	1048	1053	1058	1063	1068	1073	1078	1083	1088	1093	1098	1103	1108	1113	1118	1123	1128	1133	1138	1143	1148	1153	1158	1163	1168	1173	1178	1183	1188	1193	1198	1203	1208	1213	1218	1223	1228	1233	1238	1243	1248	1253	1258	1263	1268	1273	1278	1283	1288	1293	1298	1303	1308	1313	1318	1323	1328	1333	1338	1343	1348	1353	1358	1363	1368	1373	1378	1383	1388	1393	1398	1403	1408	1413	1418	1423	1428	1433	1438	1443	1448	1453	1458	1463	1468	1473	1478	1483	1488	1493	1498	1503	1508</
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[illegible]

[illegible]

seq decompination block:
id AAA09162 standard: DNA; 3159 bp.
XX
XX
AN AAA09162:
XX
XX
10-ABR_2000 (first entry)
XX
Human 661Ab gene, a homologue of murine EBF gene.
XX
661Ab: Transcription factor? murine EBF homologue; ETS family;
KW cytosolic; cationic; secretory; tumorigenesis; ss.
XX
XX
Itano sapientis.
OS
XX Key Location/Organisms
EH CHS 112..1014
ET /Tad a
ET misc_signal 109..115
ET /Tad b
ET /note "putative Kozak sequence"
FN W0209020584 A2.
NN
1-APR_2000.
PD
XX 02-OCT_1999: 9080 DSZ576.
XX
02-OCT_1999: 9608 OI02744.
XX
06 JUN_1999: 9005 OI04447.
XX
(ORF) DIRECTESYS INC.
FA (AFAR) AFAR D.E.
FA (MURE/) MUSEL R.S.
FA (MITC/) MITCHELL S.C.
XX
Alar DE, Hubert RS, Mitchell SC.
XX
WP1: 2030 49372.2/26.
OK P-TSDH: AA09243.
XX
Model putative transcription factor gene 661Ab for treatment,
PT diagnosis and prevention of prostate, bladder, cervical, ovarian,
PT pancreatic, and colonic cancer
PT
XX claim 4; Fig 1A: 5'UT; Ensilish.
PS
XX The human 661Ab gene encodes a putative transcription factor based on
XX homology to the murine EBF gene which encodes a transcription factor
XX which is a member of the ETS family. 661Ab is expressed in
XX androgen-dependent and androgen independent LAM prostate cancer
XX xenografts and in normal prostate at approximately equal levels. The
XX highest expression is in the prostate and colon. 661Ab may be involved
XX in activating tumor promoting genes or repressing genes that block
XX tumorogenesis. The 661Ab polynucleotides and polypeptides are used for
XX the treatment and diagnosis of cancer, e.g., prostate, bladder, cervical,
XX ovarian, pancreatic and colorectal cancer (all claimed). Anti 661Ab
XX antibodies may be used for purifying 661Ab and for isolating 661Ab
XX homologues. Antisense oligonucleotides and ribozymes can be used to
XX inhibit the transcription and translation of the 661Ab gene (claimed).
XX The 661Ab polynucleotides and polypeptides and immunogenic treatments
XX may also be used in cancer vaccines (claimed).
XX
SQ Sequence: 4159 bp; 942 A; 643 C; 684 G; 848 T; 93 other;
at least 90% GC
Qualify: 258.00 Length: 861
Ratio: 1.410 gaps: 16
Percent Similarity: 60.693 Percent Identity: 25.762
alignment block:
seq: 126, 919, 28 AAA09162

[illegible]

```

XX      23-OCT-1997;          97EP-0308450.
PR      15-Nov-1996;          GENS-0746789.
PR      31-Oct-1996;          GENS-0028791.
XX      (SMK ) SMITHKLINE BEECHAM CORP.
PA      (MON ) UNIV MONASH.
XX
PI      Deboucq C, Kola I, Tymms MJ:
EI      MPE, 1998 21:574/22.
DR      P-PDB: AAW57834.
XX
PT      New isolated polynucleotide and c-DNA, agonists and antagonists
PI      used to diagnose and treat cancer, e.g. prostate, breast, lung or
PI      epithelial tumours
PS
PS      Claim 4; Fig 1A; 3APP; English.
XX
CC      This sequence encodes the human ELF3 protein of the invention. ELF3 is
CC      used to treat patients requiring ERF by providing DNA encoding the
CC      polypeptide and expressing the polypeptide in vivo. ELF3 is used to
CC      diagnose a disease or a susceptibility to a disease related to its
CC      expression by determining a mutation in the nucleic acid sequence
CC      encoding it. The presence of ERF in a sample derived from a host can be
CC      detected. Antagonists of ELF3 are used to treat patients requiring
CC      inhibition of ELF3 polypeptide. ELF3 can be used in the early diagnosis
CC      and treatment of cancer, particularly epithelial cancer such as breast
CC      and prostate cancer.
XX
SI      Sequence 1:26-60; 4:2 A; 5:61 C; 5:60 G; 387 T; 0 others;
XX
alignment_scores:
XX      quality:    950.00           length:    429
XX      Ratio:     1.374             gaps:       17
XX      Percent similarity: 42.424   Percent identity: 22.844
XX
alignment_block:
US-09-126-945B-2 x AAV40701 ..
XX
Align seq 1/1 to: AAV40701 from: 1 to: 1920
XX
31 AAlAAIaaGyaIaVaIGlyGlugHaGaAGAsTPRSeProSerCf 47
   |||||
   ..... |||||
66 GCCTCGCCGCCTCGCTGGCAACAGCGAGACGTGGCACCGCGATACACGA 115
   |||
47 GPr..... 48
   |||
49 .... AlAtHtTrogGluGlyGlnGserAlaIleTyLeuSerTyPhe 64
   |||||
   ||| ..... |||||
116 TGCGTGCAACTGTATG..... ATTAGCAACAATTATTATCAACTACTTC 159
   ..... |||
64 AsmActLactTyTProGluAsnGsnSerSetrPalAlaAlaGlnAlaPretVal 80
   : : : : : ||| ..... |||
160 ACTTCGATGATTAAGTTCGGAGAACATTCACCTTTSCCTTTCTCTCTCTCT 209
   ..... |||
80 aSerSerArgGluGluProProGluGluProGluGlnGysProvalIleA 97
   |
210 T..... 210
97 sPSPcGlaAlaProAlaGlySerLeuAspLeuValProGlyGlyGlyThr 113
   |||
   ||| ..... |||||
211 CGCACTTTTGGGAGCAATCACTTCTCA..... CTGACC 243
   ..... |||
114 LeuGlu..... GluHisSerLeuGluGlnValGln..... SerMetValVal 127
   |||||
   : : : ||||| ..... : :
244 CGGACGACAAACCGCAATCTCATTCGACACGATACAGACAAACGACCTGCT 293
   ..... |||
127 LSTyGluValLeuLeuGlyAspPheLeuThrAlaGlyGlySylGluGluAsnIleOf 144
   : |||||

```


In vitro from yeast library vectors. ESX protein, alone and also used to screen for specific modulators, especially potential anticancer agents.

XX Sequence 1907 bp: 427 A; 557 G; 533 G; 390 T; 0 others

alignment_scores:

Quality: 246.00 Length: 419
Ratio: 1.390 Gaps: 17
Percent Similarity: 42.243 Percent Identity: 22.673

alignment_block:

US-09-126-945b-2 x AAV38355

Align seq 1/1 to: AAV38355 from: 1 to: 1907

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41 ATGAspTrpSerProSerProPro..... 48
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27 CGGAAATGGATTCTCTCGCGGCTCGCGGCTCGCGCAAGCGGACT 76
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49 .....AlaThrProGluGluGlyLeuSerA 57
   |||||
77 TGGCAATTTGGTAGGCTCAAGCTCTGAATCTGAG.....ATTAGA 120
   |||||
57 laPhetylLeuSerTyPheAspMetLeuTyPheGluAspSerSerTrp 74
   |||||
121 ACATTATTAGCACTATTCAATGGCATGTACAGCTCGAGCACTCGCACT 170
   |||||
74 AlaAlaLysAlaProGlyAlaSerSerArgGluIleProGluIlePro 90
   |||||
171 CTGGCTCTGCTTCCCTCT..... 191
   |||
90 GGLuGluGlyProValIleAspSerGlnAlaProAlaGlySerLeuAsp 107
   |||
192 .....GCCACCTTGGGCGCGGATGACT 213
   |||||
107 GGAValProGlyLeuThrPheGln.....GluHisSerProGln 171
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214 TCGTA.....CTGACCTGAGCAAGCGCGCATGTGAGAGG 254
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122 ValGln.....SerMetValValGlyValLeuLysAspIleGluThrAl 137
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255 ACAAGAAGAGCACTGCTGTTGGGAA..... 281
   |||||
137 GCGylGluGluLeuAsnIleThrAlaAspProMetAspTrpSerProSerA 154
   |||||
282 .....CAAGCTGACTGATCTGAAGAGCG 306
   |||||
154 snValGlnLysTrpLeuLeuTrp.....ThrGluHisGlnTyPheGlu 168
   |||||
307 AGGTTCGAGTGCATGAGTACCAAGTGGATGAAGCAAGTGGAGCGA 356
   |||||
169 ProProMetGlyLysAlaPheGluGluLeuLysAlaGlyGluLeuGlyAl 197
   |||||
357 AGGAAATTAATCTTCAGCAATGAGATAGGATATGAGCAATCTTCA 407
   |||||
185 dMetSerGluGluGluLeuArg.....GluArgSerProGluGlySerTy 211
   |||||
407 TTGAGCTTTGAGCACTGATCTGATCTTGGAGCTCTT 453
   |||||
201 alidHisAlaHisIleu.....AspIleTrpLysSerAla..... 212
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454 AACGCAATGCGCACTGAGAGAGCTATCTGACGCTCTCTGAGAGCT 503
   |||||
213 AlaTrpMet.....LysGluArg 218
   |||||
504 ACTTGAATATTGAGCTGTGAGCAAGAGATGATATCTTTTGAAGAG 553
   |||||
218 qThSerProGlyAlaIleHisTyPheLysAlaSerTrpSerGluGluSer 245
   |||||
554 GGTAGAGGCAAGGCGCTTTGAGCAGAGGCGGCTTGGCGCAGAGAGCT 603

```

```

225 TTTAAATGCTTTAAATGCT.....SerGlySer 245
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504 TGGAGCAGAGCTGAGTAAGGCAAGGCTTACAGCTCGGAGATGAGAG 653
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245 ..... 245
654 GGAAGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 703
245 ..... 245
704 TTTGAGAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 753
245 ..... 245
754 ATGCAATTATGAGAGCTTTGGGAGGAGATGCTTTGAGAGAGAG 803
246 .....GlyGluPro..... 248
804 AAGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 853
248 ..... 248
854 GAGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
249 .....IleHisLeuTrpGluPheLeuLysGluLeuLeuLysPro 262
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904 CGAAGAGCAGCAGCAGCTGTGAGAGTTCATTCGAGATATCCATCACT 953
263 HisSerTyGlyArgIleHisLeuAlaTrpGluAsnLysGluGluGly 279
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954 GAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
279 GlysIleGluAspSerAlaGluValAlaArgLeuTrpGlyIleAlaGly 296
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1004 CAGTCTGCTGCTGCTGAGAGCTGTGAGAGCTGAGAGCTGAGAGAG 1053
296 snAlaTrpAlaMetAspTyPheLysLeuSerArgSerIleArgGlyTr 212
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1054 AGAAGCAGCAGCAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1103
313 TTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 229
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1104 TACAAAGCAGAGATCTGGAGAGAGAGAGAGAGAGAGAGAGAG 1150
329 GlnPro 431
1151 CAGATT 1157
seq_name: 75126b/seq.dat 49-gene-seq-to-us-seq/30A030.LAT.AAC36707
seq_documentation_block:
ID AAC36707 standard: FNA: 1907 bp.
XX
XX AAC36707:
XX
XX 13-MAR-2000 (first entry)
XX
XX Nucleotide sequence for GenBank accession number 366894.
XX
XX Stimulus-regulated nucleic acid sequence profiles: nucleic acid level:
XX
XX differentially expressed nucleic acid: disease state: cancer:
XX
XX autoimmune disease: infectious disease: developmental disorder:
XX
XX proliferative disorder: neurological disorder: toxicity:
XX
XX treatment resistance: differential expression: drug discovery:
XX
XX growth factor: epidermal growth factor: radiation: stress: pathogen: ss:
XX
XX Homo sapiens.
XX
XX OS
XX PN W0995913-A2.
XX
XX 04-NOV-1999.
XX
XX 27-APR-1999. 99MO-US091119.

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[illegible]

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 76 /start 1002, 1111
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 84 /product pointed region
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 86 /product second variable region
 87 /product "Clam 8"
 88 /start 562, 714
 89 /start k
 90 /product section rich region
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 92 /product Third variable region
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 94 /start 820, 1062
 95 /start m
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[illegible][illegible]

[illegible]

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F1		/#149 4
F1	cxon	/number 2
F1		/42...526
F1		/#149 5
F1		/number 3
F1	inf room	/527...586
F1		/#149 1
F1		/number 3
F1	cxon	/587...790
F1		/#149 4
F1	inf room	/number 4
F1		/791...850
F1		/#149 1b
F1	cxon	/number 4
F1		/651...916
F1		/#149 1
F1		/number 5
F1	inf room	/917...976
F1		/#149 1
F1		/number 5
F1	cxon	/977...1042
F1		/#149 8
F1	inf room	/number 6
F1		/1043...1102
F1		/#149 1
F1	cxon	/number 6
F1		/1103...1162
F1		/#149 m
F1		/number 7
F1	inf room	/1163...1222
F1		/#149 n
F1	cxon	/number 7
F1		/1223...1270
F1		/#149 o
F1	inf room	/number 8
F1		/1271...1330
F1		/#149 p
F1	cxon	/number 8
F1		/1331...1890
F1		/#149 q
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XX		
FN	W99421549 A.	
XX		
F0	25 NOV 1993.	
XX		
F1	19 MAY 1993.	9-two-FR0044.
XX		
PR	20 MAY 1992.	92FR 0006125.
XX		
XX	(CNRS) CNRS CENT NAT RECH SE1.	
XA		
FA	Audias A., Betaille O., Desmazo C., Melot T., Peller M.	
F1	Ploastedel B., Thomas G., Zorman J.	
XX		
DK	WP1: 1993-005300/4B.	
XX	P FSB05 AA044556.	
XX		
XX	New nucleic acid of FWS gene and its hybrids) contd. gene	
F1	Sequence involved in chromosomal Translocation, also derived	
F1	mRNA, protein, fusion proteins etc., for diagnosis and treatment	
F1	of Fusing saccharide and melanoma	
PE		
XX		
XX	Disclosure: Fig 7 and Fig 14; 124pp. French.	
PS		
XX		
XX	The initial exon joins tails of the human FWS gene and the Hum F11.1	
XX	gene have been sequenced (see AA05064b and AA05066z, respectively).	
XX	The different fusion products which could be formed by fusing	
XX	exons from the two genes, as happens after specific chromosomal	
XX	translocations, can be predicted (see AA05067j, 05067h). The sequences	
XX	at translocation loci of other observed translocated genes given in	

[illegible][illegible]

XX	2/ Apr 1998	(first entry)	
XX			
XX	human TMLP2 cDNA		
XX			
KW	TMF2: sensory neuron; neurotransmitter defect;		
KW	ortholog degenerated; hearing loss; deafness; retinal dystrophy;		
KW	retinitis pigmentosa; combined rod cone dystrophy; obesity; human		
XX	animal model; transgenic animal; therapy; diagnosis; ds.		
XX			
XX	human sapiens:		
XX			
XX	Key:	locat feat/qual letters	
FT	cat	94...1656	
FT	/#1,q	a	
FT	oxon	1...92	
FT	/#1,q	b	
FT	/number	1	
FT	oxon	94...125	
FT	/#1,q	c	
FT	/number	2	
FT	oxon	129...177	
FT	/#1,q	d	
FT	/number	3	
FT	oxon	178...302	
FT	/#1,q	e	
FT	/number	4	
FT	oxon	303...441	
FT	/#1,q	f	
FT	/number	5	
FT	oxon	442...738	
FT	/#1,q	g	
FT	/number	6	
FT	oxon	739...1041	
FT	/#1,q	h	
FT	/number	7	
FT	oxon	1042...1151	
FT	/#1,q	i	
FT	/number	8	
FT	oxon	1152...1269	
FT	/#1,q	j	
FT	/number	9	
FT	oxon	1270...1368	
FT	/#1,q	k	
FT	/number	10	
FT	oxon	1369...1540	
FT	/#1,q	l	
FT	/number	11	
FT	oxon	1541...1734	
FT	/#1,q	m	
FT	/number	12	
XX			
XX	W0748004 AL		
XX			
XX	16 Oct 1997		
XX			
XX	10 Apr 1997	97MO DS05904	
XX			
XX	17 SEP 1996	96DS 0714991	
XX	10 Apr 1996	96DS 0640542	
XX	22 Aug 1996	96DS 0701480	
XX	04 SEP 1996	96DS 0706292	
XX			
XX	(JACK) JACKSON LAB		
XX	(SHEP) SHEPARD THEOPHILES INC		
XX			
XX	Myopert J., Nishida Y., Nishin T, Yan H. K., North M.		
XX			
XX	WP1: 1997_5_12642/47		
XX	P-PSDB: AAW6431		
XX			
XX	Membrane TMLP protein used for detection pro-disposition to		
XX	genetic sensory defects		

[illegible]

immunosmolality, candida, thrombolytic, coagulation, vascular, anti-thrombotic, hypotensive, decongestant, anti-immunosuppressive, anti-inflammatory, antibacterial, antiviral, antiproliferative, antithrombotic, antihypertensive, and antineoplastic. The sequences can be used for determining the presence of or predisposition to, or prevention of, or treatment of pathological conditions associated with an ORF associated disorder. The nucleotide acids can be used to express ORF proteins in gene therapy. Moreover, the proteins and nucleotide acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoporosis, arthritis, heart disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, elastic anaemia, burns, wounds, bone and cartilage damage, neuronal haemophagocytosis, anti-inflammatory disorder, to enhance coagulation, to inhibit thrombosis, and as a contraceptive.

Sequence: 1029 M; 200 A; 425 C; 224 G; 229 T; 1 other.

$$a_i = i + 1, \quad i = 1, \dots, n-1, \quad a_n = n.$$

Quality:	105.00	Length:	2.7
Ratio:	0.802	Gaps:	1.2
Percent Similarity:	43.813	Percent Identity:	21.405

all members look:

025 034 126 9431 2 X AM 7/58/75

All-in size 1/1 to: AAc75875 from: 1 to: 1024

1988年12月

ID AAC91988 standard; cDNA; 17,08 bp

Al: AM91988

20-MAK-2001 (first entry)

THE HALLMAN 7-LET CODING SEQUENCE

KW Homma, T Kot, T Iwata, and T Kikuchi in "Soluble autoimmunity of Sjögren's syndrome" *Journal of Autoimmunity* 1997; 10: 105-112

How good?

XX
DN 140300017 2454 81

07-11-07-0000

XX
DE
02 - 111N - 1496 -
66415 - 01 270445

XX
XX
WEST, J(111)-001-27/017

of factors is not a detailed modulation of individual genes, but a novel collection of a few genes of varying proportion.

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

CC The present sequence for the coding sequence for human IL-6, expressed in T cells (1-6a), encoding a protein that can be used in the treatment of autoimmune diseases associated with a Th2-type dysfunction e.g. diabetes mellitus, arthritis, multiple sclerosis, autoimmune thyroiditis, psoriasis, keratoconjunctivitis, alopecia areata, allergic responses due to arthropod bite reactions, Crohn's disease, alcoholic liver, HIV, conjoined hearts, keratoconjunctivitis, ulcerative colitis, asthma.

XX		/product	"Human D SLAM"
XX	seq pop id:	/2..157	
XX	mat pop id:	/★.91 to 158..946	
XX		/★.91 to	
XX		/product	"Mature human D SLAM"
XX	W09401B4 AL		
XX	L2 AUG 1997.		
XX	04 FEB 1997	9808 050241%.	
XX	06 FEB 1998	9808 007306Z.	
XX	19 MAR 1998	9808 007807Z.	
XX	(HOMA) HOMA CRR AB 301 TR.		
XX	Baben SM, Young D		
XX	W-1: 2000 052627/04.		
XX	P FSIHQ, AANY2479.		
XX	Now isolated dendritic enriched secreted lymphocyte activation molecules, used for treating e.g., immune disorders, cancer or inflammation, transplant rejection or infectious, or as food additives		
XX	Claim 1: Fig 1: Isotype English.		
XX	<p>This sequence represents cDNA encoding human dendritic enriched secreted lymphocyte activation molecule (D SLAM). D SLAM is homologous to members of the SLAM family and has shared here activity similar to other SLAM family members. SLAM proteins are members of the immunoglobulin superfamily and are rapidly induced after activation of naive B and T lymphocytes, causing differentiation and proliferation of immune cells. To elicit an immune response, both a secreted form of SLAM, in addition to a membrane bound SLAM, are thought to interact. Binding of D SLAM induces the production of interleukin gamma from other cell types, particularly B and T cells, because of the tissue distribution of D SLAM. This protein may also play a role in stimulate dendritic or adipo-presenting cells. The polypeptides can be used for prevent ion, treatment or ameliorating a variety of medical conditions, pathological condition or susceptibility can be diagnosed by determining the presence or amount of D SLAM polypeptides in a sample or by determining the presence of mutations in nucleotides encoding D SLAM. D SLAM proteins can be used to control the proliferation, activation, maturation, survival and/or differentiation of haematopoietic cells, in particular B and T cells. They can be used to treat immune disorders which can be genetic (such as cancer), acquired (e.g., via chemotherapy) or infection in origin. Such immune disorders include HIV infection, leukocyte adhesion deficiency syndrome, phagocytic bactericidal dysfunction or severe combined immunodeficiency (SCID). D SLAM proteins or nucleolides may be used to treat deficiencies or disorders of haematopoietic cells (e.g., anemia), and to modulate haemostatic or thrombotic activity. They may also be used in the diagnosis or treatment of autoimmune disorders such as rheumatoid arthritis, haemolytic anaemia and type I diabetes mellitus, and in the treatment of hyperproliferative disorders such as cancer. They can be used to promote neuroregeneration as a means of treating central and peripheral nervous system diseases, e.g., Alzheimer's disease, Parkinson's disease, Huntington's or mechanical and traumatic disorders (e.g., spinal cord disorders, head injury and stroke).</p>		
XX	Sequence: 4220 107; 832 A; 885 G; 755 G; 748 T; 0 others;		
al	alignment scores:		
	gap(17): 102.70	length: 339	
	ratio: 0.748	gaps: 19	
	Percent Similarity: 40.51%	Percent Identity: 23.50%	
	Alignment block:		

[illegible]

[illegible]



Alignment scores:	Quality:	299.09	Length:	211
Ratio:	2.818	Gaps:	4	
Percent similarity:	61.137	Percent identity:	33.175	
<p>Alignment block: US-09-126-9458-2 x US-09-009-913-6</p>				
<p>Align seq 1/1 Len: US-09-009-913-6 from: 1 to: 2428</p>				
135	GIUPLALALVSYSLLEUASPLICLTHALASPTROMELASPTPS	151	GIUPLALALVSYSLLEUASPLICLTHALASPTROMELASPTPS	151
136	152	152
137	153	153
138	154	154
139	155	155
140	156	156
141	157	157
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208	224	224
209	225	225
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211	227	227
212	228	228
213	229	

1	SEQUENCE FOR EACH SEQ. IS: 100: 93		
2	SEQUENCE CHARACTERISTICS:		
3	LENGTH: 1604 base pairs		
4	TYPE: nucleic acid		
5	STANDARDNESS: double		
6	TOPLOGY: linear		
7	MAPTYPE: TYPE: DNA (genomic)		
8	PERC-OS94-06251-9		
9			
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80  aserSerAacGluGluIleProGluIleProGluIleProGluValIleA 97
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210  |
97  spSerGluAlaProAlaGlySerIleAspIleValProGlyGluGlu 114
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114  GAGGlu.....GluHisSerGluGluGluIleValGlu.....SerMetValVal 127
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244  GAGAGAAATTAATGATGATGAGAGAAATTAATGAGAGAAATTAATG 293
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294  GAGGAGAA..... 400
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175  GAGGluGluAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 192
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496  AGCTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 445
192  Trp.....GluHisSerProGluGlyGlyGlyGlyGlyGlyGlyGlyGly 206
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207  AspIleGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 215
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216  ....GlyGluGluGluGluGluGluGluGluGluGluGluGluGlu 225
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593  AGCTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 642
242  Ser.....SerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 245
643  AGCTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 692
245  ....GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 245
693  GCTGATGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 742
743  GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
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793  TTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 842
246  ....GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 246
843  GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 892
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seq:documentation_block:
? Sequence 1, Application US/08368281
? Patent No. 5721113
? GENERAL INFORMATION:
? APPLICANT: Libermann, Towia A
? APPLICANT: Gortgen, Joerg P
? APPLICANT: Kunsch, Charles A
? TITLE OF INVENTION: NERF genes
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Southland Biochem Corporation
? STREET: 709 Swedland Road
? CITY: King of Prussia
? STATE: Pennsylvania
? COUNTRY: USA
? ZIP: 19406
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM pc compatible
? OPERATING SYSTEM: pc-dos/ms-dos
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/368,281
? FILING DATE:
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Baumister, Kirk
? REGISTRATION NUMBER: 33,833
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610-270-5096
? TELEFAX: 610-270-5090
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2975 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
US-08-368-281-1
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Ratio: 1.847 Gaps: 8
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240 .....Val.AspSerSerGly..... 244
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245 .....SerGlyGlnPro..... 248
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249 .....LeuHisLeuProGlnHisLeuGlnHisLeuGlnHisLeuGln 262
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279 ...PheLysIleGluAspSerAlaGlnValAlaArgLeuProGlyIle 294
1036 GAGTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
294 GAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
1086 GAAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145
311 LNTFTTLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLYSLY 327
1136 ACTATATGAAAGGATGATGATGATGATGATGATGATGATGATGAT 1182
328 ValTyrGlnHisVal 332
1183 GTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
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seq_documentation_block:
? Sequence 3, Application us/09116049A
? Patent No. 6248351
? GENERAL INFORMATION:
? APPLICANT: HUNG, Men-Chie
? TITLE OF INVENTION: HUMAN PEAK 15 A TUMOR SUPPRESSOR FOR CANCER CELLS
? FILE REFERENCE: US05582
? CURRENT APPLICATION Number: us/09116_049A
? NUMBER OF SEQ ID NOS: 11
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 3
? LENGTH: 2064
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-116-049-3
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      Ratio: 1.332      gaps: 21
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alignment_block:
us-09-126-945b-2 v us-09-116-049-3
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265 AGCAGAGACGCGCACCTCCCTACCCACCATGCGCAGCAGTCCCTTAC 314
60 usTyrThrAspMetLeuTyrProGlnAspSerSerTyrAlaAlaLysA 77

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359 CCGCTGTGGCTTGGACAGTGTGGCTGTAAAGCCCTTCCCGGGATACG 408
92 GlnCysProValIleAspSerGlnAlaProAlaGlnLysLeuAspLeuVal 108
111 :::::::::::::::::::: ::::::::::::::::::::
409 CAACGGAAATTTCTGATGATCC.....TCTGGTACCTCCGACAGCCCA 449
108 LProGlnGlnLysLeuThrLeuGlnLysLeuHisSerLeuGlnValGlnSer 125
450 CCGTGGCAAGGCTACCTCGGGGAAACATAC..... 480
125 CTValValGlnGlnValLeuLysAsnIleCysThrAlaLysLysLeuGln 141
480 ..... 480
142 AsnIleThrAlaAspProMetAspTyrSerProSerAsnValGlnLysIle 158
481 TCGCTTTCAGCAGCAGCGCTGAGACATTTGCACTCC..... 516
158 PheLeuThrProGlnHisLeuTyrArgLeuProProMetGlyLysAla 175
517 .....TTTCACTTCAGGTAAGGCGCGGAGAACCCCTGCGACGCGCT 559
175 heGlnGlnLysAlaLysLysGlnLysGlnLysAlaMetSerGlnGlnLys 191
560 ACCAAGACAGCAGCTGTGGAGCCCTGCGCCACCTATATCCAGCAGACCT 609
192 ArgGln.....ArgSerProLeu..... 197
610 AAGCAGAGATACCATGATATCCCTGATGACACGCGGCGCAGCAGCCGT 659
198 .....GlyValAspValLeuHisAlaHisLeuAspIleTyrLysSer 212
660 GAGCAGAGCGTGGG.....GCTAATGCGGACAGG.....TACCGGAGGG 697
212 LdAlaTyrProLysLysArgThr..... 219
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146  SPPTKMAASPIPTSPPTSPSTASVAIdhlystIreleuLpIh 162
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895  AGGCTGAGGATGTCG..... 911
163  GluHisGluIyArLeuLp.....ProMetGlyGly 173
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173  SALAPAGGluGluLeuAlaCysIleuGlySaluMetSerGluGlu 190
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959  CTCTATACCAATCAATCTTCAGAGGCTTCCTACCTTAACTGACAGACA 1006
190  LpPheArgIleArg..... 194
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1448  TCAAGATTCATTAATGAGTACATCAAGTACATCAAGTACATCAAGTACAT 1497
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410  GduIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 427
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1548  ATACTATATATATATATATATATATATATATATATATATATATATAT 1584
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seq_documentation_block:

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1 Sequence 1: Application US/09/213767
2 Patent No: 5948680
3 GENERAL INFORMATION:
4 APPLICANT: Brenda E. Baker
5 APPLICANT: Lex M. Gowsert
6 TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
7 FILE REFERENCE: RUS-0024
8 CURRENT APPLICATION NUMBER: US/09/213,767
9 CURRENT FILING DATE: 1998-12-17
10 NUMBER OF SEQ ID NOS: 47
11 SEQ ID NO: 1
12 LENGTH: 2266
13 TYPE: DNA
14 ORGANISM: Homo sapiens
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: (316)..(1602)
18 US-09-213-767-1

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alignment_scores:

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Quality: 225.00 Length: 168
Ratio: 2.728 Gaps: 8
Percent Similarity: 60.119 Percent Identity: 36.310

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US-09-126-945b-2 4 US-09-213-767-1 ..

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Align seq 1/1 to US-09-213-767-1 (1602) 1 to 2266

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248  TelleuHisGluIlePheArgGluArgSerProLeuIlePheIyAspVal 264
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423  GGTGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 472
298  TCAATTCATGAGGCTTCATGAGGCTTCATGAGGCTTCATGAGGCTTCAT 314
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473  CCAATATGATATACATCAAGTACATCAAGTACATCAAGTACATCAAGT 522
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570  TGCG 573

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COMPUTER READABLE FORM

; APPL. ICANT: SkolSKI, Thomas?

[illegible][illegible]


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LOCAL ID: 77..4847
INT-0593-07306-1

Alignment Scores:
Quality: 95.00 Length: 401
Ratio: 0.565 Gaps: 27
Percent Similarity: 41.895 Percent Identity: 24.439

Alignment block:
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85 .....GluProProGluIleProGly 92
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97 AspSer..... 98
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99 .....GluAlaProGlyAlaThrSerLeuAspLeu..... 107
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seq_documentation_block:
? Sequence 2: Application US/090848291A
? Patent No. 6117674
? GENERAL INFORMATION:
? APPLICANT: Ley, Sima
? APPLICANT: Pileman, Gregory D.
? APPLICANT: Schlosser, Joseph
? TITLE OF INVENTION: RICH PROTEINS AND RELATED
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 643 West Fifth Street
? STREET: Suite 4700
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071-2666
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 MB
? OPERATING SYSTEM: IBM PC, DOS 5.0
? SOFTWARE: FastSeq
? CURRENT APPLICATION DATA:
? AGENT/ATTORNEY: R/S/38/948,291A
? FILING DATE: September 26, 1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 64/027,437
? FILING DATE: October 11, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Warburg, Richard J.

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GENERAL INFORMATION:
APPLICANT: Johanna Dr. Stephen V.
APPLICANT: Van Zelle Dr. Marja
APPLICANT: Wihara Dr. Bryan M.
TITLE OF INVENTION: Amphiphotic Virus Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: 100 West Main Street
CITY: Stamford
STATE: CT
COUNTRY: United States of America
ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARC to PC software #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,719
FILING DATE: 04-JAN-1996
CLASSIFICATION: 540
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/050,684
FILING DATE: 16-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowery Dr. Karen A
REGISTRATION NUMBER: 41,474
REFERENCE/EXAMINER NUMBER: 41937-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-421-2461
TELEFAX: 203-421-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
MOLECULE TYPE: cDNA
HYDROPHILIC: No
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NAME/KEY: CDS
LOCATION: 244..2262
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Alignment scores:
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GENERAL INFORMATION:
APPLICANT: Johanna Dr. Stephen V.
APPLICANT: Van Zelle Dr. Marja
APPLICANT: Wihara Dr. Bryan M.
TITLE OF INVENTION: Amphiphotic Virus Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: 100 West Main Street
CITY: Stamford
STATE: CT
COUNTRY: United States of America
ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARC to PC software #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,719
FILING DATE: 04-JAN-1996
CLASSIFICATION: 540
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/050,684
FILING DATE: 16-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowery Dr. Karen A
REGISTRATION NUMBER: 41,474
REFERENCE/EXAMINER NUMBER: 41937-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-421-2461
TELEFAX: 203-421-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
MOLECULE TYPE: cDNA
HYDROPHILIC: No
ANTI-SENSE: No
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2262
US-08-582,719-1
Alignment scores:
Quality: 92.50 Length: 417
Ratio: 0.651 Gaps: 16
Percent similarity: 44.795 Percent identity: 21.267
Alignment blocks:
US-08-126-945b-2 & US-08-582,719-1: 1709
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REFERENCE NUMBER: 4178 0002 0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 413 4000
FAX: 703 413 2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2090 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
Topology: linear
MOLECULE TYPE: cDNA
ORGANISM: SOEBRE
ORGANISM: WISTAR RAI
TISSUE TYPE: CEREBRAL CORTEX
FEATURE:
NAME/KEY: cds
LOCATION: 156..1245
OTHER INFORMATION: /note "DEFINE METHOD: p"
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LOCATION: 252..302
OTHER INFORMATION: /note "TRANSCRIPTION DIRECTION"
OTHER INFORMATION: DEFINE METHOD:
FEATURE:
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LOCATION: 651..659
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FEATURE:
NAME/KEY: misc feature
LOCATION: 784..791
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NAME/KEY: misc feature
LOCATION: 1140..1148
OTHER INFORMATION: /note "POTENTIAL N-GLYCOSYLATION"
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aligned sequence:
quality: 91.50 length: 45
padding: 0.641 gaps: 17
percent similarity: 42.029 percent identity: 19.420
alignment block:
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seq document block:

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1 Sequence 2: Application US/08946/07A
2 Patent No. 6044084
3 GENERAL INFORMATION:
4 APPLICANT: Schindler, Matthew J.
5 APPLICANT: Chen, Yao Eseng
6 APPLICANT: Stockert, Edward J.
7 APPLICANT: Old, Lloyd J.
8 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES

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seq_name: jcrnuz_67p0p0a7q717m9b75A_17MB seq-us-08-051-7742-8
seq_documentation_block:
: Sequence 3, Application US/08051742
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OS-09-126-945B-2 x OS-08-951-742-3/rev. 11/2001
 Aligned 1/1 to reference at: OS-08-951-742-3 11/2001
 19. PROTEASIN-VALISARTAN-1,3-BIS(4-CHLOROPHENYL)-LYSINAMIDE


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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Paton's Palcos #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-500-358
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-09-500-358
FILING DATE: 28-MAR-1997
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylin, Paul I
REGISTRATION NUMBER: 36,808
FIFTEENTH/SEVENTH NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4045 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MULTIPLE TYPE: CDNA
FEATURE:
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LOCATION: 48..2786
US-09-500-358-2
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Percent Similarity: 40.13% Percent Identity: 21.78%
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Align seq 1/1 to: CELF2A3 from: 1 to: 29997

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14605 GATTCAACACATATATACAAATTGTGCAAAATTTGGCACTTCCAAATGGA 14654
143 .....IleThrAlaAspProMet 148
13655 CATTACTATGCAATAGCTGATTTATATTTTGGCTCTGATTTCTTA 13704
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13705 CCGTGGTCAATCGAGCATGGACAGATGCAATGCAAGAGATGCAATG 13754
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LOCUS XLAJ4125 1798 bp mRNA VRL 21-JAN-2000
DEFINITION Xenopus laevis ctd gene (ctd_A).
ACCESSION AJ224125
VERSION AJ224125.1 GI:5429045
KEYWORDS Ctd gene; transcription factor.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodidae; Xenopus.
REFERENCE 1 (bases 1 to 1798)
Baltzinger M., Mader Hockel A.M. and Kemp P.
XLAJ4125: expression, function and localization of a ctd gene
product for a role in endonuclear coil differentiation
Dev. Dyn. 216 (4-5): 420-433 (1999)
JOURNAL MEDLINE 20099678
AUTHORS 2 (bases 1 to 1798)
Baltzinger M.
TITLE Direct Submission
DIRECT SUBMISSION
Submitted (24-FEB-1998) Baltzinger M., Mader Hockel A.M., Kemp P.,
National de la Recherche Scientifique, 15, Rue Rene Descartes,
67084, FRANCE
FEATURES
Location/Qualifiers
1..1798

FEHHEHLEKESALHYTTEI:IIILVGEHEDVLOFZGK:WELF..*

report region 1571 - 1670
BASE COUNT 695 a 541 c 533 g 694 t
ORIGIN

alignment scores:

quality: 296.00 length: 211
ratio: 2.295 gaps: 4
percent similarity: 61.147 percent identity: 42.761

alignment block:

us-09-126-945b-2 x AF115402

Align seq 1/1 to: AF115402 from: 1 to: 2412

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seq name: gb|F01253.1
seq description: block:
locus: E01253 1447 bp DNA PAT 07 FEB 2001

REFERENCE 1 (bases 1 to 1447)
GenBank accession number: F01253.1 (11/10/2000)

VERSION E01253.1 (11/10/2000)

KEYWORDS uncloned DNA

SOURCE uncloned DNA

ORGANISM uncloned DNA

REFERENCE 1 (bases 1 to 1447)

AUTHORS

TITLE

ABSTRACT

COMMENT

FEATURES

ORIGIN

BASE COUNT

ORIGIN

BASE COUNT

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ORIGIN

[illegible]

SEQUENCE	Human: ccdline-03a: 320, cDNA to mRNA, Lambda-7.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae.
REFERENCE	1 (bases 1 to 3126)
AUTHORS	Reddy,E.S.P., Rao,V.N. and Papas,T.S.
TITLE	The era gene: A human gene related to the ets oncogene
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 84, 631-635 (1987)
MIDDLE	87317608
FEATURES	Location/Qualifiers 1..3126 organism="Homo sapiens" ab-arc="Erasn:9606" 195..1286 note="era1 protein" protein_start=1 protein_id="AAA45811.1" ab_xref="GI:182185"
CDS	/translation="MAVSLAIVAPGADTAEIMETFRETDELAVIADPTWST DVRQMLEAKFYGLDPNNILPQNIDKELFKMKLRFQRLISYNAHLISHAY LKTEPLPIITSDVDKALONSPKLMIRANDLYDEPRSAATGHRTPOSKAHS PSIVKIPEPDIDPOLDYOLIGISSIRANGSDLOLDWFLDLISNSNCSIMEZ IPCLPMHTIEVAAPFWEEFESESNNTYELSSALPYYPYINMRYVRYAFRETF RHLACALQPHDFESSITRYSDLPQESDAAGAAQNVAVQRAIPVSSPFADAN PWNSPDTGTIPENRIPLSHMSHLSGYTA"
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GENE	1 bp upstream from ERAS1 site.
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Ratio:	1.851 Gaps: 14
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US-09-126-945R-2 x HOMER011 ..	
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212 CACCCTTGCATCAGCTACACTGCGCACATCAACGCCAGACAGCATG... 257	
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329 CTATTTCTTCTTAATPrtaTrtCaTrrGAGGGGGAAGATTAAGCTTCA 378	
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429 ATGACCAAGAGATCTTCAGAAAGCTCAACCCCAAGCTAACACGGCAAT 478	
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479 GTTCTCTCACATCTGCATACCTTCAGACAGATCTCTTCTTCATAATTGA 528	
207AspLeTrpLysSer..... 211	

[illegible]

notch motifs.
JOURNAL, Mol. Cell. Biol. 13 (3), 1485-1491 (1993)
MEDLINE 94180783
COMMENT Submitted (30 SEP 1992) to EMBL by:

Japan
Phone: 045-922-1111
Fax: 045-923-0480.

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Align Seq 1/1 to: HUMF160 from: 1 to: 1781

BASE COORD	3,7221 a	3,7221 b	3,7222 a	3,7222 b	3,7223 a	3,7223 b	3,7224 a	3,7224 b	3,7225 a	3,7225 b	3,7226 a	3,7226 b	3,7227 a	3,7227 b	3,7228 a	3,7228 b	3,7229 a	3,7229 b	3,7230 a	3,7230 b	3,7231 a	3,7231 b	3,7232 a	3,7232 b	3,7233 a	3,7233 b	3,7234 a	3,7234 b	3,7235 a	3,7235 b	3,7236 a	3,7236 b	3,7237 a	3,7237 b	3,7238 a	3,7238 b	3,7239 a	3,7239 b	3,7240 a	3,7240 b	3,7241 a	3,7241 b	3,7242 a	3,7242 b	3,7243 a	3,7243 b	3,7244 a	3,7244 b	3,7245 a	3,7245 b	3,7246 a	3,7246 b	3,7247 a	3,7247 b	3,7248 a	3,7248 b	3,7249 a	3,7249 b	3,7250 a	3,7250 b	3,7251 a	3,7251 b	3,7252 a	3,7252 b	3,7253 a	3,7253 b	3,7254 a	3,7254 b	3,7255 a	3,7255 b	3,7256 a	3,7256 b	3,7257 a	3,7257 b	3,7258 a	3,7258 b	3,7259 a	3,7259 b	3,7260 a	3,7260 b	3,7261 a	3,7261 b	3,7262 a	3,7262 b	3,7263 a	3,7263 b	3,7264 a	3,7264 b	3,7265 a	3,7265 b	3,7266 a	3,7266 b	3,7267 a	3,7267 b	3,7268 a	3,7268 b	3,7269 a	3,7269 b	3,7270 a	3,7270 b	3,7271 a	3,7271 b	3,7272 a	3,7272 b	3,7273 a	3,7273 b	3,7274 a	3,7274 b	3,7275 a	3,7275 b	3,7276 a	3,7276 b	3,7277 a	3,7277 b	3,7278 a	3,7278 b	3,7279 a	3,7279 b	3,7280 a	3,7280 b	3,7281 a	3,7281 b	3,7282 a	3,7282 b	3,7283 a	3,7283 b	3,7284 a	3,7284 b	3,7285 a	3,7285 b	3,7286 a	3,7286 b	3,7287 a	3,7287 b	3,7288 a	3,7288 b	3,7289 a	3,7289 b	3,7290 a	3,7290 b	3,7291 a	3,7291 b	3,7292 a	3,7292 b	3,7293 a	3,7293 b	3,7294 a	3,7294 b	3,7295 a	3,7295 b	3,7296 a	3,7296 b	3,7297 a	3,7297 b	3,7298 a	3,7298 b	3,7299 a	3,7299 b	3,7300 a	3,7300 b	3,7301 a	3,7301 b	3,7302 a	3,7302 b	3,7303 a	3,7303 b	3,7304 a	3,7304 b	3,7305 a	3,7305 b	3,7306 a	3,7306 b	3,7307 a	3,7307 b	3,7308 a	3,7308 b	3,7309 a	3,7309 b	3,7310 a	3,7310 b	3,7311 a	3,7311 b	3,7312 a	3,7312 b	3,7313 a	3,7313 b	3,7314 a	3,7314 b	3,7315 a	3,7315 b	3,7316 a	3,7316 b	3,7317 a	3,7317 b	3,7318 a	3,7318 b	3,7319 a	3,7319 b	3,7320 a	3,7320 b	3,7321 a	3,7321 b	3,7322 a	3,7322 b	3,7323 a	3,7323 b	3,7324 a	3,7324 b	3,7325 a	3,7325 b	3,7326 a	3,7326 b	3,7327 a	3,7327 b	3,7328 a	3,7328 b	3,7329 a	3,7329 b	3,7330 a	3,7330 b	3,7331 a	3,7331 b	3,7332 a	3,7332 b	3,7333 a	3,7333 b	3,7334 a	3,7334 b	3,7335 a	3,7335 b	3,7336 a	3,7336 b	3,7337 a	3,7337 b	3,7338 a	3,7338 b	3,7339 a	3,7339 b	3,7340 a	3,7340 b	3,7341 a	3,7341 b	3,7342 a	3,7342 b	3,7343 a	3,7343 b	3,7344 a	3,7344 b	3,7345 a	3,7345 b	3,7346 a	3,7346 b	3,7347 a	3,7347 b	3,7348 a	3,7348 b	3,7349 a	3,7349 b	3,7350 a	3,7350 b	3,7351 a	3,7351 b	3,7352 a	3,7352 b	3,7353 a	3,7353 b	3,7354 a	3,7354 b	3,7355 a	3,7355 b	3,7356 a	3,7356 b	3,7357 a	3,7357 b	3,7358 a	3,7358 b	3,7359 a	3,7359 b	3,7360 a	3,7360 b	3,7361 a	3,7361 b	3,7362 a	3,7362 b	3,7363 a	3,7363 b	3,7364 a	3,7364 b	3,7365 a	3,7365 b	3,7366 a	3,7366 b	3,7367 a	3,7367 b	3,7368 a	3,7368 b	3,7369 a	3,7369 b	3,7370 a	3,7370 b	3,7371 a	3,7371 b	3,7372 a	3,7372 b	3,7373 a	3,7373 b	3,7374 a	3,7374 b	3,7375 a	3,7375 b	3,7376 a	3,7376 b	3,7377 a	3,7377 b	3,7378 a	3,7378 b	3,7379 a	3,7379 b	3,7380 a	3,7380 b	3,7381 a	3,7381 b	3,7382 a	3,7382 b	3,7383 a	3,7383 b	3,7384 a	3,7384 b	3,7385 a	3,7385 b	3,7386 a	3,7386 b	3,7387 a	3,7387 b	3,7388 a	3,7388 b	3,7389 a	3,7389 b	3,7390 a	3,7390
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|||||
5637 GAGAGTAAAGGCAAGCAAGCAAGCAATATGTCAGGCAATTCATATATCA 5668
227 .....
5687 CCAATTGAGAGGAGAGGCTTTCAGTTCAGACAGTGGATTAATGCAAAATG 5694
227 .....
5697 TATATATATATATATATATATATATATATATATATATATATATATAT 5408
228 .....
5487 CAATATATATATATATATATATATATATATATATATATATATATAT 5494
236 TheAspSer..... GluValAspSerSerGlySer 245
|||||
5437 AGCTATATATATATATATATATATATATATATATATATATATATAT 5464
245 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
5487 TCGATATATATATATATATATATATATATATATATATATATATAT 5494
252 TCGATATATATATATATATATATATATATATATATATATATATAT 272
5443 ACTGATATATATATATATATATATATATATATATATATATATATAT 5473
279 PhelGstTlenGstSperAlaGluValAlaGluValGluValGluVal 295
|||||
5496 TTTATATATATATATATATATATATATATATATATATATATATAT 5447
296 GAGATATATATATATATATATATATATATATATATATATATATAT 5472
5446 AATATATATATATATATATATATATATATATATATATATATATAT 5492
412 GTTATATATATATATATATATATATATATATATATATATATATAT 5492
5496 ATTATATATATATATATATATATATATATATATATATATATATAT 5496
429 TTTATATATATATATATATATATATATATATATATATATATATAT 5441
5443 TATATATATATATATATATATATATATATATATATATATATATAT

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seqName: qb_1n2:AE003758
seqDocument: block:
LOCUS AE003758 225092 bp DNA INV 05-01-2000
DEFINITION Drosophila melanogaster genome scaffold 1420001:225092
ACCESSION AE003758 AE002708
VERSION AE003758.2 GI:10724791
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Insecta;
Diptera; Eurytomidae; Eurytomidae; Eurytomidae;
Muscomorpha; Eurytomidae; Drosophilidae; Drosophila;
1 (bases 1 to 225092)
AUTHORS
Adams M.D., Celisken S.E., Gibbs R.A., Rubin G.M., Venturi C.J.,
Gibbs R.A., Myers E.W., Rubin G.M., and Venturi C.J.
(2000) The genome sequence of Drosophila melanogaster.
Science 287 (5461): 2185-2196 (2000)

```

Adams M.D., Celisken S.E., Gibbs R.A., Rubin G.M., Venturi C.J.,
 Gibbs R.A., Myers E.W., Rubin G.M., and Venturi C.J.
 (2000) The genome sequence of Drosophila melanogaster.
 Science 287 (5461): 2185-2196 (2000)

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(308)

gene

mRNA

source

Adams M.D., Celisken S.E., Gibbs R.A., Rubin G.M., and Venturi C.J.
 (2000) The genome sequence of Drosophila melanogaster.
 Science 287 (5461): 2185-2196 (2000)

Adams M.D., Celisken S.E., Gibbs R.A., Rubin G.M., and Venturi C.J.
 (2000) The genome sequence of Drosophila melanogaster.
 Science 287 (5461): 2185-2196 (2000)


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769 AAGAGAGAGCTTTTATGATCTGATGAGAGAGAGATGAGAGAGAA 818
217 GAGCTGTTAGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
819 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
227 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
869 TTAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
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1060 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1109
400 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
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seq name: gb|U011:AK080101

seq document ation block:
LOCATION AK080101 2948 bp DNA PAT 41-MS2-2099
DEFINITION Sequence 4 from patient US 5968734.
ACCESSION AK080101
VERSION AK080101.1 GI:10096846
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 2948)
AUTHORS Aulias A., Delatour O., Desmazes C., Melot T., Leduc M.,
Pleumastel B., Thomas G. and Zucman J.
TITLE Nucleic acid corresponding to a gene of chromosome 22 involved in
recurrent chromosomal translocations associated with the
development of cutaneous tumors, and nucleic acids of fusion
product from said translocations
PATENT US 5968734 A 3 1999 1999
FEATURES
SOURCE 1. 2948
LOCATION/FEATURES
BASE COUNT 847 a 692 c 675 g 724 t
ORIGIN
alignment scores:
gap: 1 2948
edit: 1 522
percent identity: 47.906 percent identity: 28.010

alignment block:
US 09 126 945b 2 x AK080101
align seq 1/1 for AK080101 from 1 for 2948
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163 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212

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```

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213 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
58 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 74
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75 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 90
253 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290
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441 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
113 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 117
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117 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433
441 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 490
134 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
491 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
150 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
541 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
167 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 182
591 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
183 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
641 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
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206 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206
741 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740
207 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 217
791 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
217 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
841 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
227 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
891 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 940
234 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290
941 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
290 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
988 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1034

```



```

* be preserved.
* 1784: contig of 1784 bp in length
* 1785: 1884: gap of 100 bp
* 1885: 2989: contig of 1105 bp in length
* 2990: 1089: gap of 100 bp
* 3090: 5117: contig of 2028 bp in length
* 5118: 5217: gap of 100 bp
* 5219: 5425: contig of 1406 bp in length
* 6627: 6724: gap of 100 bp
* 6727: 8933: contig of 2207 bp in length
* 8934: 9033: gap of 100 bp
* 9034: 10648: contig of 1615 bp in length
* 10649: 10748: gap of 100 bp
* 10749: 12570: contig of 1822 bp in length
* 12571: 12670: gap of 100 bp
* 12671: 15798: contig of 3128 bp in length
* 15799: 15898: gap of 100 bp
* 15899: 19125: contig of 3226 bp in length
* 19127: 19226: gap of 100 bp
* 19227: 22408: contig of 3082 bp in length
* 22409: 22408: gap of 100 bp
* 22409: 25462: contig of 3054 bp in length
* 25463: 25562: gap of 100 bp
* 25563: 29759: contig of 4196 bp in length
* 29759: 29858: gap of 100 bp
* 29859: 32899: contig of 3041 bp in length
* 32900: 32999: gap of 100 bp
* 32999: 37286: contig of 4287 bp in length
* 37287: 37386: gap of 100 bp
* 37387: 41144: contig of 3759 bp in length
* 41145: 41244: gap of 100 bp
* 41245: 46573: contig of 5429 bp in length
* 46574: 46673: gap of 100 bp
* 46674: 50564: contig of 3891 bp in length
* 50565: 50664: gap of 100 bp
* 50665: 55581: contig of 4917 bp in length
* 55582: 55681: gap of 100 bp
* 55682: 60807: contig of 5126 bp in length
* 60808: 60907: gap of 100 bp
* 60908: 65665: contig of 4659 bp in length
* 65666: 65665: gap of 100 bp
* 65667: 69423: contig of 3657 bp in length
* 69424: 69423: gap of 100 bp
* 69424: 74605: contig of 4082 bp in length
* 74606: 74605: gap of 100 bp
* 74606: 79191: contig of 5586 bp in length
* 79192: 79291: gap of 100 bp
* 79292: 84609: contig of 5318 bp in length
* 84610: 84709: gap of 100 bp
* 84710: 90445: contig of 5737 bp in length
* 90447: 90546: gap of 100 bp
* 90547: 96482: contig of 5846 bp in length
* 96483: 96482: gap of 100 bp
* 96483: 101544: contig of 5152 bp in length
* 101545: 101744: gap of 100 bp
* 101745: 108444: contig of 6710 bp in length
* 108445: 108544: gap of 100 bp
* 108545: 115975: contig of 7431 bp in length
* 115976: 116075: gap of 100 bp
* 116076: 122159: contig of 6094 bp in length
* 122160: 122269: gap of 100 bp
* 122270: 140412: contig of 8943 bp in length
* 140413: 147841: contig of 7429 bp in length
* 147842: 147941: gap of 100 bp
* 147942: 148046: contig of 10105 bp in length
* 148047: 148146: gap of 100 bp
* 148147: 157364: contig of 9218 bp in length
* 157365: 157464: gap of 100 bp
* 157465: 167083: contig of 9619 bp in length
* 167084: 167183: gap of 100 bp
* 167184: 177426: contig of 10243 bp in length
* location/Qualifiers

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1. 177426
/translation "Homo sapiens"
/3E_xref="taxon:9606"
/clone "RP11-34016"
/clone_11b="RP11 Human Male HAC"
1. 1784
/misc_feature
/note "assembly_fragment"
1895. 2989
/3E_xref="assembly_fragment"
3090. 5117
/note "assembly_fragment"
5218. 6626
/note "assembly_fragment"
6727. 8933
/note "assembly_fragment"
9034. 10648
/note "assembly_fragment"
10749. 12570
/note "assembly_fragment"
12671. 15798
/note "assembly_fragment"
15899. 19125
/note "assembly_fragment"
19227. 22408
/note "assembly_fragment"
22409. 25462
/note "assembly_fragment"
25563. 29759
/note "assembly_fragment"
29859. 32899
/note "assembly_fragment"
32900. 37286
/note "assembly_fragment"
37387. 41144
/note "assembly_fragment"
41245. 46573
/note "assembly_fragment"
46674. 50564
/note "assembly_fragment"
50665. 55581
/note "assembly_fragment"
55682. 60807
/note "assembly_fragment"
60908. 65665
/note "assembly_fragment"
65667. 69423
/note "assembly_fragment"
69424. 74605
/note "assembly_fragment"
74606. 79191
/note "assembly_fragment"
79292. 84609
/note "assembly_fragment"
vector_end:17
vector_start:1941
69424. 74605
/note "assembly_fragment"
clone_end:896
vector_start:1941
74606. 79191
/note "assembly_fragment"
79292. 84609
/note "assembly_fragment"
alignment_scores:
quality: 276.50 length: 305
ratio: 1.589 gaps: 9
Percent Similarity: 57.049 Percent Identity: 27.213
alignment_block:
US-09-126-945b-2 X AC055828
Align seq 1/1 to: AC055828 from: 1 to: 177426
60 LeuSer TyrHis AspMet LeuGly TrpProLysAspSerSerTyrAlaValLeu 76
||||| :|||||:||||| :||| :|||||
34507 TTAAGATCTCTGAAGATTTAAGCTCTGAGACATGTCAGACCTTGTAT 33556
76 SALAPROLYALASERATRAQLUUPROPIUULUPROUUGUUG 93

```


[illegible][illegible]

[illegible][illegible]

TITLE: Direct Submission
 JOURNAL: Submitted (20 Aug 1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 on Feb 16, 2000. This sequence version replaced 1:5081507.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.bcm.tmc.edu/>
 Contact: base@bcm.tmc.edu
 Project Information
 Center project name: BRAC
 Center clone name: RP198.44K7
 Summary Statistics
 Sequencing vector: M13: L08821
 Chemistry: dye primer pooling: 74% of reads
 Chemistry: dye terminator bid dye: 25% of reads
 Assembly program: Phrap: version 0.960611
 Consensus quality: 56887 bases at least Q40
 Consensus quality: 78530 bases at least Q30
 Consensus quality: 86616 bases at least Q20
 Estimated insert size: 101921; sum of counts estimation
 Quality coverage: 1x in Q20 bases; sum of counts estimation

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 69 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1461: contig of 1461 bp in length
 1462: gap of unknown length
 1482 2446: contig of 965 bp in length
 2447 2466: gap of unknown length
 2467 4289: contig of 924 bp in length
 4290 4309: gap of unknown length
 4310 4086: contig of 777 bp in length
 4087 4106: gap of unknown length
 4107 5225: contig of 1119 bp in length
 5226 5245: gap of unknown length
 5246 6428: contig of 1083 bp in length
 6429 6448: gap of unknown length
 6449 7109: contig of 761 bp in length
 7110 8387: contig of 1258 bp in length
 8388 8407: gap of unknown length
 8408 9836: contig of 1429 bp in length
 9837 9856: gap of unknown length
 9857 11460: contig of 1504 bp in length
 11461 11480: gap of unknown length
 11481 12234: contig of 854 bp in length
 12235 12254: gap of unknown length
 12255 13732: contig of 1478 bp in length
 13733 13752: gap of unknown length
 13753 14661: contig of 909 bp in length
 14662 14681: gap of unknown length
 14682 15665: contig of 984 bp in length
 15666 15685: gap of unknown length
 15686 16920: contig of 1235 bp in length
 16921 16940: gap of unknown length
 16941 17788: contig of 848 bp in length
 17789 17808: gap of unknown length
 17809 18722: contig of 914 bp in length
 18723 18742: gap of unknown length
 18743 19512: contig of 770 bp in length
 19513 19532: gap of unknown length
 19533 20676: contig of 1144 bp in length
 20677 20696: gap of unknown length
 20697 21501: contig of 805 bp in length
 21502 21521: gap of unknown length
 21522 22866: contig of 1345 bp in length

22867 22886: gap of unknown length
 22887 24258: contig of 1472 bp in length
 24259 24278: gap of unknown length
 24279 26427: contig of 204 bp in length
 26428 26447: gap of unknown length
 26448 27917: contig of 1570 bp in length
 27918 27937: gap of unknown length
 27938 28880: contig of 944 bp in length
 28881 28900: gap of unknown length
 28901 29807: contig of 907 bp in length
 29808 29827: gap of unknown length
 29828 41948: contig of 2121 bp in length
 41949 41968: gap of unknown length
 41969 43572: contig of 1604 bp in length
 43573 43592: gap of unknown length
 43593 44891: contig of 1299 bp in length
 44892 44911: gap of unknown length
 44912 46110: contig of 1199 bp in length
 46111 47688: contig of 1558 bp in length
 47689 47708: gap of unknown length
 47709 48541: contig of 834 bp in length
 48542 48561: gap of unknown length
 48562 40169: contig of 1608 bp in length
 40170 40189: gap of unknown length
 40190 41344: contig of 1155 bp in length
 41345 41364: gap of unknown length
 41365 42596: contig of 1232 bp in length
 42597 42616: gap of unknown length
 42617 44471: contig of 835 bp in length
 44472 44491: gap of unknown length
 44492 44284: contig of 813 bp in length
 44285 44304: gap of unknown length
 44305 46132: contig of 1828 bp in length
 46133 48272: gap of unknown length
 48273 48292: contig of 2120 bp in length
 48293 49747: gap of unknown length
 49748 49767: contig of 1455 bp in length
 49768 51323: contig of 1556 bp in length
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 51344 52829: contig of 1488 bp in length
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 52850 53927: contig of 1078 bp in length
 53928 53947: gap of unknown length
 53948 55806: contig of 1861 bp in length
 55807 55826: gap of unknown length
 55827 57398: contig of 1670 bp in length
 57399 57418: gap of unknown length
 57419 59461: contig of 1944 bp in length
 59462 59481: gap of unknown length
 59482 60737: contig of 1256 bp in length
 60738 60757: gap of unknown length
 60758 63029: contig of 2272 bp in length
 63030 63049: gap of unknown length
 63050 65083: contig of 2034 bp in length
 65084 65103: gap of unknown length
 65104 66948: contig of 1845 bp in length
 66949 66968: gap of unknown length
 66969 69391: contig of 2424 bp in length
 69392 69411: gap of unknown length
 69412 71348: contig of 1947 bp in length
 71349 71368: gap of unknown length
 71369 74204: contig of 2836 bp in length
 74205 74224: gap of unknown length
 74225 75348: contig of 1124 bp in length
 75349 75368: gap of unknown length
 75369 77168: contig of 1800 bp in length
 77169 78429: gap of unknown length
 78430 78449: contig of 1141 bp in length
 78450 81431: gap of unknown length
 81432 81451: gap of unknown length

[illegible]

Accession	Source	Organism	Accession	Source	Organism
202	EMBL	Homo sapiens	219	EMBL	Homo sapiens
44016	EMBL	Homo sapiens	242	EMBL	Homo sapiens
44018	EMBL	Homo sapiens	243	EMBL	Homo sapiens
234	EMBL	Homo sapiens	244	EMBL	Homo sapiens
44098	EMBL	Homo sapiens	245	EMBL	Homo sapiens
230	EMBL	Homo sapiens	246	EMBL	Homo sapiens
44198	EMBL	Homo sapiens	247	EMBL	Homo sapiens
44218	EMBL	Homo sapiens	248	EMBL	Homo sapiens
277	EMBL	Homo sapiens	249	EMBL	Homo sapiens
44298	EMBL	Homo sapiens	250	EMBL	Homo sapiens
293	EMBL	Homo sapiens	251	EMBL	Homo sapiens
44348	EMBL	Homo sapiens	252	EMBL	Homo sapiens
310	EMBL	Homo sapiens	253	EMBL	Homo sapiens
44398	EMBL	Homo sapiens	254	EMBL	Homo sapiens
327	EMBL	Homo sapiens	255	EMBL	Homo sapiens
44445	EMBL	Homo sapiens	256	EMBL	Homo sapiens


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250  .....Hislofip 252
740  CTCCTACACCTCCACACCAAAAGACACACACACACACACCTACAG 779
253  GCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
780  GATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 829
269  CATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 286
840  AAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 879
286  TTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 302
860  CATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 929
303  ASPATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 319
940  GAAAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 979
419  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 341
980  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1013
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seq document ation block:
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VERSION    AK10483.1      GI:12615071
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1. (bases 1 to 5510)
            Brooks Wilson, A. R., Buckler, A., Cardon, L., Carey, A., Daly, M.,
            Miller, A., and North, M.
            Ascid related genes
            JOURNAL   Patient: US 6087485, A 3 11 JUN 2000;
            FEATURES   Location/Genotype
            SOURCE     1. 5510
            ORGANISM   /Organism "unknown"
FASTA COUNT 1424 a 1064 c 1191 g 1631 t
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          Ref: 1.497              Gaps: 13
          Percent Similarity: 53.191 Percent Identity: 25.228
alignment block:
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85  ATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 192
1  TTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1
202  GCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 248
102  GATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 114
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249  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298
119  .....GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 128

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345  TAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 361
371  .....GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
192  TTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 177
416  CTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
178  .....TCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAAT 194
466  GCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515
193  TCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAAT 205
516  GCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565
207  .....ASPATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 212
566  AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
212  GATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 224
616  CATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 665
225  .....Hislofip 249
666  AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
240  TTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 247
713  TTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
248  .....Protein
763  TCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAAT 812
250  .....Hislofip 252
813  GCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
253  GCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
863  GATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 912
269  CATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 286
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913  AAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 962
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963  CATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1012
303  ASPATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 319
1013  GAAAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1062
419  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 341
1063  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
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seq document ation block:
LOCUS      DROEF248      5475 bp      mRNA
DEFINITION Drosophila melanogaster E74B protein.
ACCESSION  M37083

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VERSION      AF045527.1  GI:418929
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SOURCE       Mus musculus
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 1419)
AUTHORS     Herbert, M.A., Kleinbaum, L.A., Sun, L.Y., and Burton, F.H.
TITLE       Molecular cloning and expression of Ebf, a new member of the ets
            transcription factor/oncogene gene family
JOURNAL      98262938
MEDLINE     2 (bases 1 to 1419)
AUTHORS     Herbert, M.A., Kleinbaum, L.A., Sun, L.Y., and Burton, F.H.
TITLE       Direct Submission
SUBMITTER    Submitted (21-NOV-1997) Pharma-Pharm, University of Minnesota, 405
            Delaware St., SE, 5-249 Millard Hall, Minneapolis, MN 55455, USA
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            144..1046
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            IHQVWYVQWFMQIHL;PNDILASQ;PPEPFI;SPEH;QSSSL;QEFPAAS;AQ
            LYSNHLQANWQ;SSSL;EUSAHNV;KTEETES;IMWEL;ENNY;DYSYS;VIL
            LDK;PFCRAQISMT;SRI;PASFQNMK;PQD;HVKSH;TKKH;N;H;H;M;E;F;E;L;L;E
            SID;RQFI;E;M;E;R;S;T;P;P;P;S;E;A;V;A;G;I;W;P;P;S;S;V;P;S;A;M;P;Y;T;E;R;E;L
            EVAD;R;P;I;V;E;R;K;A;R;W;P;E;N;P;E;N;
BASE COUNT   497 a      309 c      299 g      314 t
ORIGIN
different_scores:
            quality: 256 50      length: 246
            ratio: 1.914      gaps: 9
            percent similarity: 54.472      percent identity: 28.949
alignment_block:
US_09-126-945b-2 x AF045527
Alignment 1/1 for AF045527 from 1 to 1419
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242  GCTCATATATGACCAATACATCTGAGATGGTGAAGAGCTTCT 341
||||| ||||| ||||| ||||| |||||
163  GHSGLHLYAVATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 179
||||| ||||| ||||| ||||| |||||
342  GATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 401
||||| ||||| ||||| ||||| |||||
178  GATAGAGLGLYSGLHLYAVATGCTGCTGCTGCTGCTGCTGCT 304
||||| ||||| ||||| ||||| |||||
362  TTAAGAGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
||||| ||||| ||||| ||||| |||||
195  GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
||||| ||||| ||||| ||||| |||||
442  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461
||||| ||||| ||||| ||||| |||||
207  ASPIPTSPPTSCASVAGLGLYSIPRAAGLIPPLHRL 244
||||| ||||| ||||| ||||| |||||
482  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
||||| ||||| ||||| ||||| |||||
214  TPTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
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542  TCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
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242  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
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623  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
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247  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
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673  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
||||| ||||| ||||| ||||| |||||
248  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
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723  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772
||||| ||||| ||||| ||||| |||||
252  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
||||| ||||| ||||| ||||| |||||
773  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
||||| ||||| ||||| ||||| |||||
264  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
||||| ||||| ||||| ||||| |||||
823  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
||||| ||||| ||||| ||||| |||||
286  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
||||| ||||| ||||| ||||| |||||
873  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
||||| ||||| ||||| ||||| |||||
402  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
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923  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
||||| ||||| ||||| ||||| |||||
419  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
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973  GATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1007
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seq_name: qb_p5:AF124439
seq_documentation_block:
LUTUS      AF124439      mRNA      27-JAN-2000
DEFINITION Homo sapiens transcript (us-09-126-945b-2) (USP-3) mRNA, complete cds.
VERSION    AF124439
KEYWORDS   AF124439.1  BL4838433
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 2586)
AUTHORS   Kas, K., Pharo, E., Hall, E., Gu, X., Akbari, Y., Katsaxoglou, A., Garg, P., Kapeller, R., and Kleinbaum, L.A.
TITLE     USP-3, a novel member of an opitrium specific ets transcription factor subfamily, demonstrates different target gene specificity from ESE-1
JOURNAL    J. Biol. Chem. 275 (4): 2986-2998 (2000)
MEDLINE   20112876
REFERENCE  2 (bases 1 to 2586)
AUTHORS   Kas, K., Pharo, E., Hall, E., Gu, X., Akbari, Y., Katsaxoglou, A., Garg, P., Kapeller, R., and Kleinbaum, L.A.
TITLE     Direct Submission
SUBMITTER  Submitted (28-NOV-1999) to the NIH, for use in the Human Genome Project, 340 Brookline Ave., Boston, MA 02115, USA
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            /misc_feature="prostate gland"
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            /gene="USP-3"

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[illegible]

Journal Patient: US 5744039 A 43 31 MAR 1998
 FEATURES Location/Qualities
 Source: Location "unknown"
 NAME: count 418 a 443 c 408 t 435 t
 ORIGIN

alignment scores:
 quality: 251.50 length: 550
 penalty: 1.251 gaps: 22
 percent similarity: 47.92% percent identity: 21.69%

alignment block:
 US 09 126 945b 2 x 196206

Align seq 1/1 for 196206 from 1 to 1604

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40  GATGASPTTpsrtrpsrtrpsrtrpsrtrpsrtrpsrtrpsrtrps 57
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46  CGAGGCGGGCGGGCGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGG  67
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
57  Lrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrly  73
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88  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
74  AlAAAla...lyslAArlyl...AlAsrSGAsrlylgnrlylgnrly  89
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100  AGTGGCGGGCGGGCGAGCGGGCGGGCGGGCGGGCGGGCGGGCGAA 119
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87  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
150  TTTGATTTTGGAAAGATGGATTTTGGATTTTGGATTTTGGATTTT 179
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94  S...P 94
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200  TACTAAATCTCAATAAAATAAAATAAAATAAAATAAAATAAAATA 249
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94  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 107
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250  CAGCGCGGGCGGGCGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 269
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450  CAGCGCGGGCGGGCGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 499
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159  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 184
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549  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
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594  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 643
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199  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 210
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644  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 693
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SGLAAATrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 219
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694  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 743
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220  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 240
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744  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 793
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230  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 235
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794  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 843
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235  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
844  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 893
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259  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
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994  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1043
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247  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1044  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1093
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
247  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1094  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1143
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
247  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1144  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1193
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
247  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1194  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1243
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
248  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1244  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1293
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
254  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 269
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1294  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1340
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
270  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 286
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1341  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1387
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
286  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 303
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1388  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1437
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
403  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 419
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1438  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1487
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
420  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 442
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1488  rVAlrlylgnrlylgnrlylgnrlylgnrlylgnrlylgnrlylgn 1524
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

```

seq_name: qb_pa; hst:ETSL

Section 10: Certification Block:

LOCUS	SIZE(bp)	PROBE	DATE
DEFINITION	Human DNA for c-fos-1 proto-oncogene.	PK1	24-MAR-1993

ADDITION	X14/98
VERSION	X14798.1 01:298M1

KEYWORDS: alternative splicing; c-ets-1 gene; c-ets-1 proto-oncogene; oncogene; proto-oncogene.

CHRISTIANISM Homo sapiens

Elkai'ood; P
Mammalia; P

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HEALTHREFS

[illegible][illegible]


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649 ..... 654
105 LeuAspIleuValProGlyValGluThrLeuGluGluHisSerLeuGluGlu 121
111 .....
654 PEGAAAGCTGCTCTGACGGCTTCACAAAACAAAGAG ..... 689
121 GATGCTGAGCTGAGValValGlyValValLeuGlyAspLeuGluThrAlaG 148
689 ..... 689
148 YSLYSLeuLeuAsnLeuThrAlaAspProMetAspTrpSerProAsn 154
154 .....
690 ...CAGCGACCTGGGAATTCGAAACACGCGCGACATCGACAAACGACG 747
155 ValGluHisTrpLeuLeuTrpThrGluHisGluTyrAlaGluProGlu 171
171 .....
171 GCGLYGAlaPheGluGlu.....LeuAlaGlyLysLeuGlyAlaGlu 186
186 .....
186 AGCTGTGAGATTTCACAAAGCTTCGACAGCGGAGACATGGTGCTGCT 191
782 AGCTGTGAGATTTCACAAAGCTTCGACAGCGGAGACATGGTGCTGCT 191
186 GATSerGluGluIlePheMetGluHisSerPro.....LeuGlyLysVal 201
842 TCGCTAAACCAATGCTTCCTGACCTGACCTCGACACTTGGTGGGCAATG 191
202 LeuHisAlaHisLeuAspLeuLeuLysSerAlaGluLeuPheLeuLysGlu 216
882 CTGCGGAGACATCAACAAATCTGAG.....AAGAGAGAG 216
218 GTHSerPro.....GlyAla..... 224
917 TCGAAACATATACAGGTAATGAGCTGACCTACCTACCAATGCT 224
224 .....GlySer 227
967 GTTAACTTCGATTAATTGATGATGATGATGATGATGATGATGATGAT 1016
228 AlaSerThrSerGlu.....GluSerTrp..... 245
1017 GTTCTCTGCTCAAGATCTCGACAGAGCAACTTCATGCAAGATCTATCA 1066
245 ..... 245
1067 GATCTTCTATCTATGATTCGAAACAAATTCCTGCTCTCAAGATCA 1116
246 .....ThrAspSer..... 248
1117 AGTATTAATCTTCTGATCTTCAGAGATCTGCTCAAGATGATGATGAT 1166
249 .....GluVal.....AspSerSer 244
1167 CAAATCAATTAATCTTCTGATCAAGCAAGAGCGTAACTCGACAAATCA 1216
244 TCTSSCTGCGlu..... 247
1217 GTGCTTGGGAGAGCTACCTGCGTAAATTCGAGGAGCAAGATCTTTTG 1266
247 ..... 247
1267 AAGAGCTTAATCAATCAATTAATTTTAACTGAGCTGACAGCTGAGG 1316
247 ..... 247
1317 AAGCAATTAATCTTCAGACAGCTGAGAGAGAGAGAGAGAGAGAGAG 1366
247 ..... 247
1367 CAGACTAAGAGATTAATCTGATTCGCTGAGAGAGAGAGAGAGAGAG 1416
247 ..... 247

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1417 CTTTCAGAGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1466
248 .....ProLeuGlu 250
1467 GGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1516
250 SLeuTrpGluGluGluLysLeuGluGluGluGluGluGluGluGluGlu 267
1517 GCTGTGAGAGATTCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
267 GATPheLeuMetGluAsnLysLeuGlyLeuGluGlyLysLeuGluAsp 284
1564 CTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1610
284 SerAlaGluValAlaGluGluTrpGlyLeuAlaLysAsnAlaGluAlaPhe 400
1611 CCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1660
400 TAspTrpAspLysLeuSerAlaGluGluGluGluGluGluGluGluGlu 417
1661 GAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1710
417 LeuLeuAspLysProAspLeuSerGluAlaGluValTyrGluIleVal 442
1711 TATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1764

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